

SYN-128.ST25.txt  
SEQUENCE LISTING

<110> Zeneca Limited

<120> Insecticidal Proteins from Paecilomyces and Synergistic  
Combinations Thereof

<130> SYN-128

<140> US 10/019,823

<141> 2001-12-21

<150> PCT/GB00/02457

<151> 2000-06-23

<150> GB 9915215.9

<151> 1999-06-29

<150> GB 9930536.9

<151> 1999-12-23

<160> 65

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 33

<212> PRT

<213> Paecilomyces sp.

<220>

<221> VARIANT

<222> 1, 2

<223> Xaa = Any Amino Acid

<400> 1

Xaa	Xaa	Ile	Cys	Thr	Pro	Ala	Gly	Val	Lys	Cys	Pro	Ala	Ala	Leu	Pro
1				5					10					15	
Cys	Cys	Pro	Gly	Leu	Arg	Cys	Ile	Gly	Gly	Val	Asn	Asn	Lys	Val	Cys
			20					25					30		

Arg

<210> 2

<211> 33

<212> PRT

<213> Paecilomyces sp.

<400> 2

Gly	Lys	Ile	Cys	Thr	Pro	Ala	Gly	Val	Lys	Cys	Pro	Ala	Ala	Leu	Pro
1				5					10					15	
Cys	Cys	Pro	Gly	Leu	Arg	Cys	Ile	Gly	Gly	Val	Asn	Asn	Lys	Val	Cys
			20					25					30		

Arg

<210> 3

<211> 35

<212> PRT

<213> Paecilomyces sp.

SYN-128.ST25.txt

<220>

<221> VARIANT

<222> 1, 2

<223> Xaa = Any Amino Acid

<400> 3

Xaa Xaa Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala  
 1 5 10 15  
 Leu Pro Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys  
 20 25 30  
 Val Cys Arg  
 35

<210> 4

<211> 332

<212> DNA

<213> Paecilomyces sp.

<400> 4

ggcaagatct gcactcctgc tggagttgta cgtattttca tccatttcct ycaccactcc 60  
 tctaacaatga agcaactttc tcttctctct agaaatgtcc cgcggctctt ccttgctgcc 120  
 ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tggatctggc aagcgagacc 180  
 ataacatgac gcagtatact aaccctggcc gttatagaac aagggttgga gtcgacatgt 240  
 tktacaacct ctacaaacgc gcgcactaat gacaacggta gtgccggtaa ttctagtgtc 300  
 gcaacttttg agcgtgggat aagtatgctt cg 332

<210> 5

<211> 320

<212> DNA

<213> Paecilomyces sp.

<400> 5

gggaaaaatt gtacgccggc ggggggttgta cgtatttctca tccatttcct ccaccactcc 60  
 tctaacaatga agcaactctc tcttctctct agaaatgtcc cgcggctctt ccttgctgcc 120  
 ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tcctgacacg acgtgaaggc 180  
 aatgtactga ccctggccgt tatagaacaa ggttgtagt cgacatgttt tacaacctct 240  
 acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300  
 cgtgggataa gtatgcttcg 320

<210> 6

<211> 320

<212> DNA

<213> Paecilomyces sp.

<400> 6

gggaaaaatt gtacgccggc ggggggttgta cgtatttctca tccatttcct ccaccactcc 60  
 tctaacaatga agcaactctc tcttctctct araaatgtcc cgcggctctt ccttgctgcc 120  
 ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tcctgacacg acgtgaaggc 180  
 aatgtactga ccctggccgt tatagaacaa ggttgtagt cgacatgttt tacaacctct 240  
 acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300  
 cgtgggataa gtatgcttcg 320

<210> 7

<211> 174

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic polynucleotide codon optimised

<400> 7

atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60  
 Page 2

SYN-128.ST25.txt

gagatccagg ccggcaagat ctgcaccccg gccggcgtga agtgcccggc cgccctccc 120  
tgctgcccgg gcctccgctg catcggcggc gtgaacaaca aggtgtgccg ctga 174

<210> 8

<211> 174

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide codon optimised

<400> 8

atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60  
gagatccagg ccggtaaaat ttgtaccccg gccggcgtga agtgcccggc cgccctccc 120  
tgttgtccgg gcctcaggtg tattggtggg gtgaataata aagtgtgtcg ctga 174

<210> 9

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence containing intron sequence

<400> 9

atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60  
gagatccagg ccggcaagat ctgcactcct gctggagtgg tttgtttctg cttctacctt 120  
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180  
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240  
ttaatttata actttttctaa tatatgacca aaacatgggt atgttttagaa atgtcccgcg 300  
gctcttcctt gctgccccgg acttcgctgc atcggcggcg tcaacaacaa ggtttgccgg 360  
taa 363

<210> 10

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 10

atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60  
gagatccagg cctcctacgg caagatctgc actcctgctg gagttgtttg tttctgcttc 120  
tacctttgat atatatataa taattatcat taattagtag taatataata tttcaaata 180  
ttttttcaaa ataaaagaat gtagtatata gcaattgctt ttctgtagtt tataagtgtg 240  
tatattttta tttataactt ttctaataata tgaccaaacc atgggtgatgt ttagaaatgt 300  
cccgcggctc ttccttgctg ccccggaact cgctgcatcg gcggcgtcaa caacaaggtt 360  
tgccgggtaa 369

<210> 11

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 11

atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60  
gagatccagg cctcctacat ctgcactcct gctggagtgg tttgtttctg cttctacctt 120  
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180  
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240

SYN-128.ST25.txt

```
ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa atgtcccgcg 300
gctcttcctt gctgcccccg acttcgctgc atcggcggcg tcaacaacaa ggtttgcccg 360
taa 363
```

<210> 12  
 <211> 363  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic sequence containing intron and codon optimised

```
<400> 12
atgggtggca gcggcagggc tgctctgctg ctggcccttg tggccgtgag cctggccgtg 60
gagatccagg ccggaagat ctgcaccccg gccggcggtg tttgtttctg cttctacctt 120
tgatataat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa gtgcccggcc 300
gcctccccgt gctgccccgg cctccgctgc atcggcggcg tgaacaacaa ggtgtgccgc 360
tga 363
```

<210> 13  
 <211> 439  
 <212> DNA  
 <213> Paecilomyces sp.

```
<400> 13
tctacttctt catctcacgc catatatcct cccaaaatca cacctcttcc ttcaccatgc 60
aaatctccgc cgtcattgtc gcactcttct ccagcgccgc catggccggc aagatctgca 120
ctcctgctgg agttgtacgt attttcattc atttcctyca ccactcctct aacatgaagc 180
aactttctct tctctctaga aatgtcccg cgcctcttct tgctgccccg gacttcgctg 240
catcgccggc gtcaacgtaa gtcaccatgg atctggcaag cgagaccata acatgacgca 300
gtatactaac cctggccggt atagaacaag gttgtgagtc gacatgttkt acaacctcta 360
caaacgcgcg cactaatgac aacggtagtg ccggaattc tagtgtcgca acttttgagc 420
gtgggataag tatgcttgc 439
```

<210> 14  
 <211> 102  
 <212> DNA  
 <213> Paecilomyces sp.

```
<400> 14
ggcaagatct gcactcctgc tggagttaaa tgtcccgcg ctcttccttg ctgccccgga 60
cttcgctgca tcggcggcgt caacaacaag gtttgccggt aa 102
```

<210> 15  
 <211> 84  
 <212> DNA  
 <213> Dahlia sp.

```
<400> 15
atgggttaata gatctgttgc tttttctgct tttgttctta ttctttttgt tttggctatt 60
tcagatatgt ctctgttttc agga 84
```

<210> 16  
 <211> 87  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Radish signal sequence

SYN-128.ST25.txt

<400> 16  
atggctaagt ttgcttctat tattgctctt ttgtttgctg cacttgtttt gtttgctgca 60  
tttgaagctc caactatggt tgaagct 87

<210> 17  
<211> 72  
<212> DNA  
<213> Zea mays

<400> 17  
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60  
gagatccagg cc 72

<210> 18  
<211> 90  
<212> DNA  
<213> Nicotiana sp.

<400> 18  
atgggatttg ttctcttttc acaattgcct tcatttcttc ttgtctctac acttctctta 60  
ttcctagtaa tatccactc ttgccgtgcc 90

<210> 19  
<211> 51  
<212> DNA  
<213> Paecilomyces sp.

<400> 19  
atgcaaatct ccgccgtcat tgtcgcactc ttcgccagcg ccgccatggc c 51

<210> 20  
<211> 28  
<212> PRT  
<213> Dahlia sp.

<400> 20  
Met Val Asn Arg Ser Val Ala Phe Ser Ala Phe Val Leu Ile Leu Phe  
1 5 10 15  
Val Leu Ala Ile Ser Asp Ile Ala Ser Val Ser Gly  
20 25

<210> 21  
<211> 29  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Radish protein target sequence

<400> 21  
Met Ala Lys Phe Ala Ser Ile Ile Ala Leu Leu Phe Ala Ala Leu Val  
1 5 10 15  
Leu Phe Ala Ala Phe Glu Ala Pro Thr Met Val Glu Ala  
20 25

<210> 22  
<211> 24  
<212> PRT  
<213> Zea Mays

<400> 22

SYN-128.ST25.txt

Met Gly Gly Ser Gly Arg Ala Ala Leu Leu Leu Ala Leu Val Ala Val  
 1 5 10 15  
 Ser Leu Ala Val Glu Ile Gln Ala  
 20

<210> 23  
 <211> 30  
 <212> PRT  
 <213> Nicotiana sp.

<400> 23  
 Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser  
 1 5 10 15  
 Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala  
 20 25 30

<210> 24  
 <211> 17  
 <212> PRT  
 <213> Paecilomyces sp.

<400> 24  
 Met Gln Ile Ser Ala Val Ile Val Ala Leu Phe Ala Ser Ala Ala Met  
 1 5 10 15  
 Ala

<210> 25  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primers

<400> 25  
 tcgggctcgc atgaattcgc ggccgcattt tttttttttt tttt 44

<210> 26  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primers

<400> 26  
 tcgggctcgc atgaattcg 19

<210> 27  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primers

<400> 27  
 atgaattcgc ggccgcat 18

<210> 28  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primers  
  
 <400> 28  
 tcgggctcgc atgaattcgc g 21  
  
 <210> 29  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primers  
  
 <400> 29  
 ctcgcatgaa ttcgcggccg c 21  
  
 <210> 30  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primers  
  
 <221> misc\_feature  
 <222> 9, 12, 15  
 <223> n = A,T,C or G  
  
 <400> 30  
 athtgyacnc cngcngg 17  
  
 <210> 31  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primers  
  
 <221> misc\_feature  
 <222> 9, 12, 15, 18  
 <223> n = A,T,C or G  
  
 <400> 31  
 athtgyacnc cngcnggngt 20  
  
 <210> 32  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primers  
  
 <221> misc\_feature  
 <222> 3, 6, 9, 12, 15  
 <223> n = A,T,C or G

<400> 32  
 acnccngcng gngtnaa 17  
 <210> 33  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Primers  
 <221> misc\_feature  
 <222> 3, 12, 15  
 <223> n = A,T,C or G  
 <400> 33  
 ccntgytgyc cnggnyt 17  
 <210> 34  
 <211> 16  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Primers  
 <221> misc\_feature  
 <222> 2, 14  
 <223> n = A,T,C or G  
 <400> 34  
 tnaartgyat hggngg 16  
 <210> 35  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Primers  
 <221> misc\_feature  
 <222> 3, 6, 18  
 <223> n = A,T,C or G  
 <400> 35  
 ggngtnaaya ayaargtntg 20  
 <210> 36  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Primers  
 <221> misc\_feature  
 <222> 12, 15, 18, 21, 24  
 <223> n = inosine  
 <400> 36  
 aarathtgya cncnccngg ngtnaa 26



<210> 37  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primers

<221> misc\_feature  
 <222> 3, 6, 9, 12, 21, 24  
 <223> n = inosine

<400> 37  
 ccngcnggng tnaartgycc ngcngc

26

<210> 38  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primers

<221> misc\_feature  
 <222> 6, 9, 12, 15, 18  
 <223> n = inosine

<400> 38  
 tgyccngcng cnytnccntg ytgycc

26

<210> 39  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primers

<221> misc\_feature  
 <222> 9, 12, 15  
 <223> n = inosine

<400> 39  
 tgyathggng gngtnaayaa yaargt

26

<210> 40  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primers

<400> 40  
 taaatgtccc gcggctcttc c

21

<210> 41  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Primers  
 <400> 41  
 cggctcttcc ttgctgcccc g 21  
 <210> 42  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Primers  
 <400> 42  
 tgctgccccg gacttcgctg c 21  
 <210> 43  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Primers  
 <221> misc\_feature  
 <222> 23, 24, 25, 26, 27  
 <223> n = A,T,C or G  
 <400> 43  
 ggtttaatta cccaagtttg agnnnnn 27  
 <210> 44  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Primers  
 <400> 44  
 ctcaaacttg ggtaattaaa cc 22  
 <210> 45  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Primers  
 <400> 45  
 ggtttaatta cccaagtt 18  
 <210> 46  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Primers  
 <400> 46  
 taattacca agtttgag 18

<210> 47  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primers  
  
 <400> 47  
 ggtttaatta cccaagtttg ag 22  
  
 <210> 48  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primers  
  
 <221> misc\_feature  
 <222> 3, 15, 18, 21  
 <223> n = inosine  
  
 <400> 48  
 canacyttrt trttnacncc ncc 23  
  
 <210> 49  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primers  
  
 <400> 49  
 atgcagcgaa gtccggggca g 21  
  
 <210> 50  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primers  
  
 <400> 50  
 ggggcagcaa ggaagagccg c 21  
  
 <210> 51  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primers  
  
 <400> 51  
 aagagccgcg ggacatttaa c 21  
  
 <210> 52  
 <211> 49  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 52

agttaaattgt cccgcggctc ttccttgctg ccccgactt cgctgcatc

49

<210> 53

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 53

gatgcagcga agtccggg

18

<210> 54

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ia1 Emb1. Accession No. X62821

<221> VARIANT

<222> 602

<223> Xaa = Any Amino Acid

<400> 54

```

Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1      5      10      15
Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20      25      30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
 35      40      45
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50      55      60
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65      70      75      80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85      90      95
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
100      105      110
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
115      120      125
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
130      135      140
Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
145      150      155      160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
165      170      175
Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
180      185      190
Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
195      200      205
Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
210      215      220
Val Glu Arg Ala Gly Asp Tyr Ser Tyr His Cys Val Lys Trp Tyr Ser
225      230      235      240
Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg

```

## 250

$\langle 210 \rangle$	55
$\langle 211 \rangle$	719

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PROTEIN cry1Ia2 Embl. Accession No. M98544

&lt;400&gt; 55

```

Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1      5      10      15
Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20      25      30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
 35      40      45
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50      55      60
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65      70      75      80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85      90      95
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
100      105      110
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
115      120      125
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
130      135      140
Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
145      150      155      160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
165      170      175
Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
180      185      190
Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
195      200      205
Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
210      215      220
Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser
225      230      235      240
Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
245      250      255
Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
260      265      270
Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
275      280      285
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
290      295      300
Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
305      310      315      320
Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
325      330      335
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
340      345      350
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
355      360      365
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
370      375      380
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
385      390      395      400
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
405      410      415
Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
420      425      430
Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln
435      440      445

```

SYN-128.ST25.txt

Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro  
 450 455 460  
 Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser  
 465 470 475 480  
 Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala  
 485 490 495  
 Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu  
 500 505 510  
 Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro  
 515 520 525  
 Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe  
 530 535 540  
 Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg  
 545 550 555 560  
 Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser  
 565 570 575  
 Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn  
 580 585 590  
 Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr  
 595 600 605  
 Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala  
 610 615 620  
 Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe  
 625 630 635 640  
 Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala  
 645 650 655  
 Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu  
 660 665 670  
 Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val  
 675 680 685  
 Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe  
 690 695 700  
 Glu Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met  
 705 710 715

<210> 56  
 <211> 719  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PROTEIN cry1Ia3 Embl. Accession No. L36338

<400> 56  
 Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala  
 1 5 10 15  
 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile  
 20 25 30  
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr  
 35 40 45  
 Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile  
 50 55 60  
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly  
 65 70 75 80  
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys  
 85 90 95  
 Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile  
 100 105 110  
 Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu  
 115 120 125  
 Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser  
 130 135 140

SYN-128.ST25.txt

Trp	Val	Gly	Asn	Arg	Asn	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Lys	Ser
145					150					155					160
Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe
				165					170					175	
Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Leu	Pro	Ile	Tyr	Ala	Gln	Ala
			180					185					190		
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Lys
		195					200					205			
Glu	Trp	Gly	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln
	210					215					220				
Val	Glu	Arg	Ala	Gly	Asp	Tyr	Ser	Tyr	His	Cys	Val	Lys	Trp	Tyr	Ser
225					230					235					240
Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Glu	Ser	Trp	Val	Arg
				245						250				255	
Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val
			260					265					270		
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Gln	Met	Tyr	Pro	Ile	Lys	Thr	Thr
		275					280					285			
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His
	290					295					300				
Pro	His	Pro	Ser	Phe	Thr	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro
305					310					315					320
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Val	Arg	Asn	Pro	His	Leu	Leu
				325					330					335	
Asp	Phe	Leu	Glu	Gln	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser
			340					345					350		
Asn	Thr	Gln	Tyr	Met	Asn	Met	Trp	Gly	Gly	His	Lys	Leu	Glu	Phe	Arg
		355					360					365			
Thr	Ile	Gly	Gly	Thr	Leu	Asn	Ile	Ser	Thr	Gln	Gly	Ser	Thr	Asn	Thr
	370					375					380				
Ser	Ile	Asn	Pro	Val	Thr	Leu	Pro	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg
385					390					395					400
Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val	Asn
				405					410					415	
Gly	Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Val	Thr	His	Pro	Ile
			420					425					430		
Ala	Ser	Asp	Asn	Phe	Tyr	Tyr	Pro	Gly	Tyr	Ala	Gly	Ile	Gly	Thr	Gln
		435					440					445			
Leu	Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Ala	Thr	Gly	Gln	Pro
	450					455					460				
Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser
465					470					475					480
Ala	Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala
				485					490					495	
Asp	Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu
			500					505					510		
Val	Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro
		515					520					525			
Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe
	530					535					540				
Gly	Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg
545					550					555					560
Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser
				565					570					575	
Ile	Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn
			580					585					590		
Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Arg	Thr	Val	Gly	Phe	Thr
		595					600					605			
Thr	Pro	Phe	Ser	Phe	Leu	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala
	610					615					620				
Trp	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe
625					630					635					640
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala



SYN-128.ST25.txt

Gln	Glu	Lys	Val	645	Thr	Ala	Leu	Phe	Thr	650	Ser	Thr	Asn	Pro	Arg	655	Gly	Leu
Lys	Thr	Asp	Val	660	Lys	Asp	Tyr	His	Ile	665	Asp	Gln	Val	Ser	Asn	670	Leu	Val
Glu	Ser	Leu	Ser	675	Asp	Glu	Phe	Tyr	Leu	680	Asp	Glu	Lys	Arg	Glu	Leu	Phe	
Glu	Ile	Val	Lys	690	Tyr	Ala	Asn	Glu	Leu	700	Ile	Glu	Arg	Asn	Met			
705					710					715								

<210> 57  
 <211> 719  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PROTEIN cry1Ia4 Embl. Accession No. L49391

<400> 57

Met	Lys	Leu	Lys	Asn	Gln	Asp	Lys	His	Gln	Ser	Phe	Ser	Ser	Asn	Ala			
1				5					10					15				
Lys	Val	Asp	Lys	Ile	Ser	Thr	Asp	Ser	Leu	Lys	Asn	Glu	Thr	Asp	Ile			
			20					25					30					
Glu	Leu	Gln	Asn	Ile	Asn	His	Glu	Asp	Cys	Leu	Lys	Met	Ser	Glu	Tyr			
		35					40					45						
Glu	Asn	Val	Glu	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile			
	50				55						60							
Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly			
65					70					75					80			
Gln	Val	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys			
			85						90					95				
Gly	Lys	Asn	Gln	Trp	Glu	Ile	Phe	Met	Glu	His	Val	Glu	Glu	Ile	Ile			
		100						105					110					
Asn	Gln	Lys	Ile	Ser	Thr	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Thr	Asp	Leu			
		115					120					125						
Lys	Gly	Leu	Gly	Asp	Ala	Leu	Ala	Val	Tyr	His	Asp	Ser	Leu	Glu	Ser			
	130					135					140							
Trp	Val	Gly	Asn	Arg	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Lys	Ser				
145					150				155					160				
Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe			
			165						170					175				
Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Pro	Ile	Tyr	Ala	Gln	Ala				
		180						185				190						
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Lys			
	195							200				205						
Glu	Trp	Gly	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln			
	210					215					220							
Val	Glu	Arg	Ala	Gly	Asp	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Ser			
	225				230					235					240			
Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Glu	Ser	Trp	Val	Arg			
			245						250					255				
Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val			
		260						265					270					
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Gln	Met	Tyr	Pro	Ile	Lys	Thr	Thr			
	275						280					285						
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His			
	290					295					300							
Pro	His	Pro	Ser	Phe	Thr	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro			
	305				310					315				320				
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Val	Arg	Asn	Pro	His	Leu	Leu			
			325						330					335				
Asp	Phe	Leu	Glu	Gln	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser			

SYN-128.ST25.txt

```

340
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
355
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
370
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
385
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
405
Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
420
Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Val Gly Ile Gly Thr Gln
435
Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro
450
Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
465
Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
485
Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
500
Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
515
Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
530
Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
545
Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
565
Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
580
Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr
595
Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
610
Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
625
Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala
645
Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu
660
Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val
675
Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe
690
Glu Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met
705
710
715

```

<210> 58

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ia5 Embl. Accession No. Y08920

<400> 58

```

Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
1      5      10      15
Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
20      25      30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr

```

SYN-128.S123.txt																
Glu 35	Asn 50	Val 65	Glu 80	Pro 95	Phe 110	Val 125	Ser 140	Ala 155	Ser 170	Thr 185	Ile 200	Gln 215	Thr 230	Gly 245	Ile 260	Gly 275
Gly 65	Ile 80	Ala 95	Gly 110	Lys 125	Ile 140	Leu 155	Gly 170	Thr 185	Leu 200	Gly 215	Val 230	Pro 245	Phe 260	Ala 275	Gly 290	Lys 305
Gln 80	Val 95	Ala 110	Ser 125	Leu 140	Tyr 155	Ser 170	Phe 185	Ile 200	Met 215	Glu 230	Glu 245	Leu 260	His 275	Val 290	Pro 305	Lys 320
Gly 95	Lys 110	Asn 125	Gln 140	Trp 155	Glu 170	Ile 185	Leu 200	Phe 215	Arg 230	Glu 245	His 260	Val 275	Glu 290	Thr 305	Ala 320	Ile 335
Asn 110	Gln 125	Lys 140	Ile 155	Ser 170	Thr 185	Tyr 200	Ala 215	Arg 230	Asn 245	Lys 260	Ala 275	Leu 290	Thr 305	Asp 320	Leu 335	Ser 350
Lys 125	Gly 140	Leu 155	Gly 170	Asp 185	Ala 200	Leu 215	Ala 230	Val 245	Tyr 260	His 275	Asp 290	Ser 305	Leu 320	Glu 335	Thr 350	Ser 365
Trp 140	Val 155	Gly 170	Asn 185	Arg 200	Asn 215	Asn 230	Thr 245	Arg 260	Ala 275	Arg 290	Ser 305	Val 320	Val 335	Arg 350	Ser 365	Phe 380
Gln 155	Tyr 170	Ile 185	Ala 200	Leu 215	Leu 230	Leu 245	Met 260	Phe 275	Val 290	Gln 305	Lys 320	Leu 335	Pro 350	Ser 365	Ser 380	Phe 395
Ala 170	Val 185	Ser 200	Gly 215	Glu 230	Glu 245	Val 260	Pro 275	Leu 290	Leu 305	Pro 320	Ile 335	Tyr 350	Ala 365	Gln 380	Ala 395	Ile 410
Ala 185	Asn 200	Leu 215	His 230	Leu 245	Leu 260	Leu 275	Leu 290	Arg 305	Asp 320	Ala 335	Ser 350	Ile 365	Phe 380	Gly 395	Lys 410	Lys 425
Glu 200	Trp 215	Gly 230	Leu 245	Ser 260	Ser 275	Ser 290	Glu 305	Ile 320	Ser 335	Thr 350	Phe 365	Tyr 380	Asn 395	Arg 410	Val 425	Gln 440
Val 215	Glu 230	Arg 245	Ala 260	Gly 275	Asp 290	Tyr 305	Ser 320	Asp 335	His 350	Cys 365	Val 380	Lys 395	Trp 410	Tyr 425	Ser 440	Ser 455
Thr 230	Gly 245	Leu 260	Asn 275	Asn 290	Leu 305	Arg 320	Gly 335	Thr 350	Asn 365	Ala 380	Glu 395	Ser 410	Trp 425	Val 440	Val 455	Arg 470
Tyr 245	Asn 260	Gln 275	Phe 290	Arg 305	Arg 320	Asp 335	Met 350	Thr 365	Leu 380	Met 395	Val 410	Leu 425	Asp 440	Leu 455	Val 470	Val 485
Ala 260	Leu 275	Phe 290	Pro 305	Ser 320	Tyr 335	Asp 350	Thr 365	Gln 380	Met 395	Tyr 410	Pro 425	Ile 440	Lys 455	Thr 470	Thr 485	Thr 500
Ala 275	Gln 290	Leu 305	Thr 320	Arg 335	Glu 350	Val 365	Tyr 380	Thr 395	Thr 410	Asp 425	Ala 440	Ile 455	Gly 470	Thr 485	Val 500	His 515
Pro 305	His 320	Pro 335	Ser 350	Phe 365	Thr 380	Ser 395	Thr 410	Thr 425	Trp 440	Tyr 455	Trp 470	Asn 485	Asn 500	Ala 515	Pro 530	Pro 545
Ser 320	Phe 335	Ser 350	Ala 365	Ile 380	Glu 395	Ala 410	Ala 425	Val 440	Val 455	Arg 470	Asn 485	Pro 500	His 515	Pro 530	Leu 545	Leu 560
Asp 335	Phe 350	Leu 365	Glu 380	Gln 395	Val 410	Thr 425	Ile 440	Tyr 455	Ser 470	Leu 485	Leu 500	Ser 515	Ser 530	Arg 545	Trp 560	Ser 575
Asn 350	Thr 365	Gln 380	Tyr 395	Met 410	Asn 425	Met 440	Trp 455	Gly 470	Gly 485	His 500	Lys 515	Leu 530	Glu 545	Phe 560	Arg 575	Arg 590
Thr 365	Ile 380	Gly 395	Gly 410	Thr 425	Leu 440	Asn 455	Ile 470	Ser 485	Thr 500	Gln 515	Gly 530	Ser 545	Thr 560	Asn 575	Thr 590	Thr 605
Ser 385	Ile 395	Asn 410	Pro 425	Val 440	Thr 455	Thr 470	Pro 485	Phe 500	Thr 515	Ser 530	Arg 545	Leu 560	Thr 575	Ala 590	Val 605	Ala 620
Thr 395	Glu 410	Ser 425	Leu 440	Ala 455	Gly 470	Leu 485	Asn 500	Leu 515	Phe 530	Leu 545	Gln 560	Thr 575	Val 590	Pro 605	Val 620	Ala 635
Gly 410	Val 425	Pro 440	Arg 455	Val 470	Val 485	Phe 500	His 515	Trp 530	Lys 545	Phe 560	Val 575	Thr 590	His 605	Pro 620	Pro 635	Ile 650
Ala 425	Ser 440	Asp 455	Asn 470	Phe 485	Tyr 500	Tyr 515	Pro 530	Gly 545	Tyr 560	Ala 575	Gly 590	Ile 605	Gly 620	Thr 635	Gln 650	Gln 665
Leu 440	Gln 455	Asp 470	Ser 485	Glu 500	Asn 515	Glu 530	Leu 545	Pro 560	Pro 575	Glu 590	Ala 605	Ile 620	Thr 635	Gly 650	Gln 665	Pro 680
Asn 465	Tyr 480	Glu 495	Ser 510	Tyr 525	Ser 540	His 555	Arg 570	Leu 585	Ser 600	His 615	Ile 630	Gly 645	Leu 660	Ile 675	Ser 690	Ser 705
Ala 480	Ser 495	His 510	Val 525	Lys 540	Ala 555	Leu 570	Val 585	Tyr 600	Ser 615	Trp 630	Thr 645	His 660	Arg 675	Ser 690	Ser 705	Ala 720
Asp 495	Arg 510	Thr 525	Asn 540	Thr 555	Ile 570	Glu 585	Pro 600	Asn 615	Ser 630	Ile 645	Thr 660	Gln 675	Ile 690	Pro 705	Leu 720	Leu 735
Val 510	Lys 525	Ala 540	Phe 555	Asn 570	Leu 585	Ser 600	Ser 615	Gly 630	Ala 645	Ala 660	Val 675	Val 690	Arg 705	Gly 720	Pro 735	Pro 750
Gly 525	Phe 540	Thr 555	Gly 570	Gly 585	Asp 600	Ile 615	Leu 630	Arg 645	Arg 660	Thr 675	Asn 690	Thr 705	Gly 720	Thr 735	Phe 750	Phe 765

SYN-128.ST25.txt

Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg  
 545 550 555 560  
 Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser  
 565 570 575  
 Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn  
 580 585 590  
 Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr  
 595 600 605  
 Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala  
 610 615 620  
 Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe  
 625 630 635 640  
 Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala  
 645 650 655  
 Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu  
 660 665 670  
 Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val  
 675 680 685  
 Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe  
 690 695 700  
 Glu Ile Val Lys Tyr Ala Asn Glu Leu His Ile Glu Arg Asn Met  
 705 710 715

<210> 59

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ib1 Emb1. Accession No. U07642

<400> 59

Met Lys Leu Lys Asn Pro Asp Lys His Gln Ser Leu Ser Ser Asn Ala  
 1 5 10 15  
 Lys Val Asp Lys Ile Ala Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile  
 20 25 30  
 Glu Leu Lys Asn Met Asn Asn Glu Asp Tyr Leu Arg Met Ser Glu His  
 35 40 45  
 Glu Ser Ile Asp Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile  
 50 55 60  
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly  
 65 70 75 80  
 Gln Ile Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys  
 85 90 95  
 Gly Lys Ser Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile  
 100 105 110  
 Asn Gln Lys Ile Leu Thr Tyr Ala Arg Asn Lys Ala Leu Ser Asp Leu  
 115 120 125  
 Arg Gly Leu Gly Asp Ala Leu Ala Val Tyr His Glu Ser Leu Glu Ser  
 130 135 140  
 Trp Val Glu Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Asn  
 145 150 155 160  
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe  
 165 170 175  
 Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala  
 180 185 190  
 Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys  
 195 200 205  
 Glu Trp Gly Leu Ser Ala Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln  
 210 215 220  
 Val Glu Arg Thr Arg Asp Tyr Ser Asp His Cys Ile Lys Trp Tyr Asn  
 225 230 235 240

SYN-128.ST25.txt

Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Lys	Ser	Trp	Val	Arg
				245					250					255	
Tyr	Asn	Gln	Phe	Arg	Lys	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val
			260					265					270		
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Leu	Val	Tyr	Pro	Ile	Lys	Thr	Thr
		275					280					285			
Ser	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His
	290					295					300				
Pro	Asn	Gln	Ala	Phe	Ala	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro
305					310					315					320
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Ile	Arg	Ser	Pro	His	Leu	Leu
				325					330					335	
Asp	Phe	Leu	Glu	Lys	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser
			340					345					350		
Asn	Thr	Gln	Tyr	Met	Asn	Met	Trp	Gly	Gly	His	Arg	Leu	Glu	Ser	Arg
		355					360					365			
Pro	Ile	Gly	Gly	Ala	Leu	Asn	Thr	Ser	Thr	Gln	Gly	Ser	Thr	Asn	Thr
	370					375					380				
Ser	Ile	Asn	Pro	Val	Thr	Leu	Gln	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg
385					390					395					400
Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val	Asn
				405					410					415	
Gly	Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Pro	Thr	Leu	Pro	Ile
			420					425					430		
Ala	Ser	Asp	Asn	Phe	Tyr	Tyr	Leu	Gly	Tyr	Ala	Gly	Val	Gly	Thr	Gln
		435					440					445			
Leu	Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Thr	Thr	Gly	Gln	Pro
	450					455					460				
Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser
465					470					475					480
Ala	Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala
				485					490					495	
Asp	Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu
			500					505					510		
Val	Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro
		515					520					525			
Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe
					535						540				
Gly	Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg
545					550					555					560
Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser
				565					570					575	
Ile	Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn
			580					585					590		
Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Arg	Thr	Ile	Gly	Phe	Thr
		595					600					605			
Thr	Pro	Phe	Ser	Phe	Ser	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala
		610				615					620				
Trp	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe
625					630					635					640
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala
				645					650					655	
Gln	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu
			660					665					670		
Lys	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val
		675					680					685			
Glu	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe
	690					695					700				
Glu	Ile	Val	Lys	Tyr	Ala	Lys	Gln	Ile	His	Ile	Glu	Arg	Asn	Met	
705					710					715					

SYN-128.ST25.txt

<211> 33  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> PROTEIN

<221> VARIANT  
<222> 1, 2, 3, 5, 6, 7, 8, 9, 10, 12, 13, 14, 15, 16, 19, 20, 21,  
22, 24, 25, 26, 27, 28, 29, 30, 31, 33  
<223> Xaa = Any Amino Acid

<400> 60  
Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa  
1 5 10 15  
Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys  
20 25 30  
Xaa

<210> 61  
<211> 439  
<212> DNA  
<213> Paecilomyces sp.

<400> 61  
tctacttctt catctcacgc catatatcct cccaaaatca cacctcttcc ttcaccatgc 60  
aaatctccgc cgtcattgtc gcactcttcg ccagcgccgc catggccggc aagatctgca 120  
ctcctgctgg agttgtacgt attttcatcc atttcctyca ccactcctct aacatgaagc 180  
aactttctct tctctctaga aatgtcccgc ggctcttctc tgctgccccg gacttcgctg 240  
catcgccggc gtcaacgtaa gtcaccatgg atctggcaag cgagaccata acatgacgca 300  
gtatactaac cctggccggt atagaacaag gttgtgagtc gacatgttkt acaacctcta 360  
caaacgcgcg cactaatgac aacggtagtg ccggaattc tagtgctgca acttttgagc 420  
gtgggataag tatgcttcg 439

<210> 62  
<211> 438  
<212> DNA  
<213> Paecilomyces sp.

<400> 62  
attacccaag tttgagggca ttcaatttca cacagtctca cgctttcgac gcatctactt 60  
cttcgtctca cgccatatat cctcccaaaa tcacacctct tccttcacca tgcaaatctc 120  
cgccgtcatt gtcgcactct tcgccagcgc cgccatggcc ggcaagatct gcactcctgc 180  
tggagttaaa tgtcccgcgg ctcttccttg ctgccccgga cttcgctgca tcggcggcgt 240  
caacaacaag gtttgccggt aattctagtg tcgcaacttt tgagcgtggg ataagtatgc 300  
ttcgttcggt gtatggagtt ctctcccgga gttaagctc ggccggtcga cagcgggtct 360  
gctatacttg atcttiacagc gatactattg atagaaatgc acatcttcat tcatgctgca 420  
tgaaaaaaa aaaaaaaa 438

<210> 63  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> INSECTICIDAL PROTEIN MOTIF

<400> 63  
Leu Pro Cys Cys Pro Gly  
1 5

<210> 64  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> INSECTICIDAL PROTEIN MOTIF  
 <400> 64  
 Ile Cys Thr Pro Ala  
 1 5

<210> 65  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> PROTEIN REGION N-TERMINAL  
 <221> VARIANT  
 <222> 1, 2  
 <223> Xaa = Any Amino Acid  
 <400> 65  
 Xaa Xaa Ile Cys Thr  
 1 5